

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/763,985A

DATE: 11/25/2001

TIME: 14:05:11

Input Set : A:\0020-4817P.ST25.txt

Output Set: N:\CRF3\11212001\I763985A.raw

3 <110> APPLICANT: ITOH, Kyogo et al.  
 5 <120> TITLE OF INVENTION: NOVEL TUMOR ANTIGEN PROTEIN SART-13 AND TUMOR ANTIGEN  
 PEPTIDES THEREOF

7 &lt;130&gt; FILE REFERENCE: 0020-4817P

9 &lt;140&gt; CURRENT APPLICATION NUMBER: 09/763,985A

10 &lt;141&gt; CURRENT FILING DATE: 2001-02-28

12 &lt;160&gt; NUMBER OF SEQ ID NOS: 64

14 &lt;170&gt; SOFTWARE: PatentIn version 3.1

16 &lt;210&gt; SEQ ID NO: 1

17 &lt;211&gt; LENGTH: 3798

18 &lt;212&gt; TYPE: DNA

19 &lt;213&gt; ORGANISM: Homo sapiens

21 &lt;220&gt; FEATURE:

22 &lt;221&gt; NAME/KEY: CDS

23 &lt;222&gt; LOCATION: (12)..(2900)

24 &lt;223&gt; OTHER INFORMATION:

27 &lt;400&gt; SEQUENCE: 1

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29	Met Ala Thr Ala Ala Glu Thr Ser Ala Ser Glu Pro Glu	
30	1 5 10	
32	gct gag tcc aag gct ggg ccc aag gct gac gga gag gat gag gtt	98
33	Ala Glu Ser Lys Ala Gly Pro Lys Ala Asp Gly Glu Glu Asp Glu Val	
34	15 20 25	
36	aag gcg gct agg aca agg aga aag gtg tta tcg cgg gct gtg gcc gct	146
37	Lys Ala Ala Arg Thr Arg Arg Lys Val Leu Ser Arg Ala Val Ala Ala	
38	30 35 40 45	
40	gcg aca tac aag acc atg ggg cca gcg tgg gat cag cag gag gaa ggc	194
41	Ala Thr Tyr Lys Thr Met Gly Pro Ala Trp Asp Gln Gln Glu Glu Gly	
42	50 55 60	
44	gtg agc gag agc gat ggg gat gag tac gcc atg gct tcc tcc gcg gag	242
45	Val Ser Glu Ser Asp Gly Asp Glu Tyr Ala Met Ala Ser Ser Ala Glu	
46	65 70 75	
48	agc tcc ccc ggg gag tac gag tgg gaa tat gac gaa gag gag gag aaa	290
49	Ser Ser Pro Gly Glu Tyr Glu Trp Glu Tyr Asp Glu Glu Glu Glu Lys	
50	80 85 90	
52	aac cag ctg gag att gag aga ctg gag gag cag ttg tct atc aac gtc	338
53	Asn Gln Leu Glu Ile Glu Arg Leu Glu Glu Gln Leu Ser Ile Asn Val	
54	95 100 105	
56	tat gac tac aac tgc cat gtg gac ttg atc aga ctg ctc agg ctg gaa	386
57	Tyr Asp Tyr Asn Cys His Val Asp Leu Ile Arg Leu Leu Arg Leu Glu	
58	110 115 120 125	
60	ggg gag ctt acc aag gtg agg atg gcc cgc cag aag atg agt gaa atc	434
61	Gly Glu Leu Thr Lys Val Arg Met Ala Arg Gln Lys Met Ser Glu Ile	
62	130 135 140	
64	ttt ccc ttg act gaa gag ctc tgg ctg gag tgg ctg cat gac gag atc	482
65	Phe Pro Leu Thr Glu Glu Leu Trp Leu Glu Trp Leu His Asp Glu Ile	
66	145 150 155	
68	agc atg gcc cag gat ggc ctg gac aga gag cac gtg tat gac ctc ttt	530

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Input Set : A:\0020-4817P.ST25.txt

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70			160					165					170				
72	gag	aaa	gcc	gtg	aag	gat	tac	att	tgt	cct	aac	att	tgg	cta	gag	tat	578
73	Glu	Lys	Ala	Val	Lys	Asp	Tyr	Ile	Cys	Pro	Asn	Ile	Trp	Leu	Glu	Tyr	
74		175					180				185						
76	ggc	cag	tac	tca	gtt	ggt	ggg	att	ggt	cag	aaa	ggt	ggc	ctt	gag	aaa	626
77	Gly	Gln	Tyr	Ser	Val	Gly	Gly	Ile	Gly	Gln	Lys	Gly	Gly	Leu	Glu	Lys	
78	190					195					200				205		
80	gtt	cgc	tcc	gtg	ttt	gaa	agg	gct	ctc	tcg	tct	gtt	ggt	tta	cat	atg	674
81	Val	Arg	Ser	Val	Phe	Glu	Arg	Ala	Leu	Ser	Ser	Val	Gly	Leu	His	Met	
82				210						215				220			
84	acc	aaa	gga	ctc	gcc	ctc	tgg	gag	gct	tac	cga	gag	ttt	gaa	agt	gcg	722
85	Thr	Lys	Gly	Leu	Ala	Leu	Trp	Glu	Ala	Tyr	Arg	Glu	Phe	Glu	Ser	Ala	
86			225					230					235				
88	att	gtg	gaa	gct	gct	cgg	ctt	gag	aaa	gtc	cac	agt	ctt	ttc	cgg	cga	770
89	Ile	Val	Glu	Ala	Ala	Arg	Leu	Glu	Lys	Val	His	Ser	Leu	Phe	Arg	Arg	
90		240					245					250					
92	cag	ttg	gcg	atc	cca	ctc	tat	gat	atg	gag	gcc	aca	ttt	gca	gag	tat	818
93	Gln	Leu	Ala	Ile	Pro	Leu	Tyr	Asp	Met	Glu	Ala	Thr	Phe	Ala	Glu	Tyr	
94		255				260				265							
96	gaa	gaa	tgg	tca	gaa	gac	cca	ata	cca	gag	tca	gta	att	cag	aac	tat	866
97	Glu	Glu	Trp	Ser	Glu	Asp	Pro	Ile	Pro	Glu	Ser	Val	Ile	Gln	Asn	Tyr	
98	270			275						280				285			
100	aac	aaa	gca	cta	cag	cag	ctg	gag	aaa	tat	aaa	ccc	tat	gaa	gaa	gca	914
101	Asn	Lys	Ala	Leu	Gln	Gln	Leu	Glu	Lys	Tyr	Lys	Pro	Tyr	Glu	Glu	Ala	
102			290							295				300			
104	ctg	ttg	cag	gca	gag	gca	cca	agg	ctg	gca	gaa	tat	caa	gca	tat	atc	962
105	Leu	Leu	Gln	Ala	Glu	Ala	Pro	Arg	Leu	Ala	Glu	Tyr	Gln	Ala	Tyr	Ile	
106			305					310					315				
108	gat	ttt	gag	atg	aaa	att	ggc	gat	cct	gct	cgc	att	cag	ttg	atc	ttt	1010
109	Asp	Phe	Glu	Met	Lys	Ile	Gly	Asp	Pro	Ala	Arg	Ile	Gln	Leu	Ile	Phe	
110		320				325						330					
112	gag	cgc	gcc	ctg	gtc	gag	aac	tgc	ctt	gtc	cca	gac	tta	tgg	atc	cgt	1058
113	Glu	Arg	Ala	Leu	Val	Glu	Asn	Cys	Leu	Val	Pro	Asp	Leu	Trp	Ile	Arg	
114		335				340					345						
116	tac	agt	cag	tac	cta	gat	cga	caa	ctg	aaa	gta	aag	gat	ttg	gtt	tta	1106
117	Tyr	Ser	Gln	Tyr	Leu	Asp	Arg	Gln	Leu	Lys	Val	Lys	Asp	Leu	Val	Leu	
118	350				355					360				365			
120	tct	gta	cat	aac	cgc	gct	att	aga	aac	tgc	ccc	tgg	aca	gtt	gcc	tta	1154
121	Ser	Val	His	Asn	Arg	Ala	Ile	Arg	Asn	Cys	Pro	Trp	Thr	Val	Ala	Leu	
122			370						375					380			
124	tgg	agt	cgg	tac	ctc	ttg	gcc	atg	gag	aga	cat	gga	gtt	gat	cat	caa	1202
125	Trp	Ser	Arg	Tyr	Leu	Leu	Ala	Met	Glu	Arg	His	Gly	Val	Asp	His	Gln	
126			385					390					395				
128	gta	att	tct	gta	acc	ttc	gag	aaa	gct	ttg	aat	gcc	ggc	ttc	atc	cag	1250
129	Val	Ile	Ser	Val	Thr	Phe	Glu	Lys	Ala	Leu	Asn	Ala	Gly	Phe	Ile	Gln	
130		400				405						410					
132	gcc	act	gat	tat	gtg	gag	att	tgg	cag	gca	tac	ctt	gat	tac	ctg	agg	1298
133	Ala	Thr	Asp	Tyr	Val	Glu	Ile	Trp	Gln	Ala	Tyr	Leu	Asp	Tyr	Leu	Arg	

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134	415	420	425	
136	aga agg gtt gat ttc aaa caa gac tcc agt aaa gag ctg gag gag ttg			1346
137	Arg Arg Val Asp Phe Lys Gln Asp Ser Ser Lys Glu Leu Glu Glu Leu			
138	430	435	440	445
140	agg gcc gcc ttt act cgt gcc ttg gag tat ctg aag cag gag gtg gaa			1394
141	Arg Ala Ala Phe Thr Arg Ala Leu Glu Tyr Leu Lys Gln Glu Val Glu			
142		450	455	460
144	gag cgt ttc aat gag agt ggt gat cca agc tgc gtg att atg cag aac			1442
145	Glu Arg Phe Asn Glu Ser Gly Asp Pro Ser Cys Val Ile Met Gln Asn			
146		465	470	475
148	tgg gct agg att gag gct cga ctg tgc aat aac atg cag aaa gct cgg			1490
149	Trp Ala Arg Ile Glu Ala Arg Leu Cys Asn Asn Met Gln Lys Ala Arg			
150		480	485	490
152	gaa ctc tgg gat agc atc atg acc aga gga aat gcc aag tac gcc aac			1538
153	Glu Leu Trp Asp Ser Ile Met Thr Arg Gly Asn Ala Lys Tyr Ala Asn			
154		495	500	505
156	atg tgg cta gag tat tac aac ctg gaa aga gct cat ggt gac acc cag			1586
157	Met Trp Leu Glu Tyr Tyr Asn Leu Glu Arg Ala His Gly Asp Thr Gln			
158	510	515	520	525
160	cac tgc cgg aag gct ctg cac cgg gcc gtc cag tgc acc agt gac tac			1634
161	His Cys Arg Lys Ala Leu His Arg Ala Val Gln Cys Thr Ser Asp Tyr			
162		530	535	540
164	cca gag cac gtc tgc gaa gtg tta ctc acc atg gag agg aca gaa ggt			1682
165	Pro Glu His Val Cys Glu Val Leu Leu Thr Met Glu Arg Thr Glu Gly			
166		545	550	555
168	tct tta gaa gat tgg gat ata gct gtt cag aaa act gaa acc cga tta			1730
169	Ser Leu Glu Asp Trp Asp Ile Ala Val Gln Lys Thr Glu Thr Arg Leu			
170		560	565	570
172	gct cgt gtc aat gag cag aga atg aag gct gca gag aag gaa gca gcc			1778
173	Ala Arg Val Asn Glu Gln Arg Met Lys Ala Ala Glu Lys Glu Ala Ala			
174		575	580	585
176	ctt gtg cag caa gaa gaa gaa aag gct gaa caa cgg aaa aga gct cgg			1826
177	Leu Val Gln Gln Glu Glu Lys Ala Glu Gln Arg Lys Arg Ala Arg			
178	590	595	600	605
180	gct gag aag aaa gcg tta aaa aag aag aaa aag atc aga ggc cca gag			1874
181	Ala Glu Lys Lys Ala Leu Lys Lys Lys Lys Lys Ile Arg Gly Pro Glu			
182		610	615	620
184	aag cgc gga gca gat gag gac gat gag aaa gag tgg ggc gat gat gaa			1922
185	Lys Arg Gly Ala Asp Glu Asp Asp Glu Lys Glu Trp Gly Asp Asp Glu			
186		625	630	635
188	gaa gag cag cct tcc aaa cgc aga agg gtc gag aac agc atc cct gca			1970
189	Glu Glu Gln Pro Ser Lys Arg Arg Arg Val Glu Asn Ser Ile Pro Ala			
190		640	645	650
192	gct gga gaa aca caa aat gta gaa gta gca gca ggg ccc gct ggg aaa			2018
193	Ala Gly Glu Thr Gln Asn Val Glu Val Ala Ala Gly Pro Ala Gly Lys			
194		655	660	665
196	tgt gct gcc gta gat gtg gag ccc cct tcg aag cag aag gag aag gca			2066
197	Cys Ala Ala Val Asp Val Glu Pro Pro Ser Lys Gln Lys Glu Lys Ala			
198	670	675	680	685

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200	gcc	tcc	ctg	aag	agg	gac	atg	ccc	aag	gtg	ctg	cac	gac	agc	agc	aag	2114
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202				690						695					700		
204	gac	agc	atc	acc	gtc	ttt	gtc	agc	aac	ctg	ccc	tac	agc	atg	cag	gag	2162
205	Asp	Ser	Ile	Thr	Val	Phe	Val	Ser	Asn	Leu	Pro	Tyr	Ser	Met	Gln	Glu	
206				705					710					715			
208	ccg	gac	acg	aag	ctc	agg	cca	ctc	ttc	gag	gcc	tgt	ggg	gag	gtg	gtc	2210
209	Pro	Asp	Thr	Lys	Leu	Arg	Pro	Leu	Phe	Glu	Ala	Cys	Gly	Glu	Val	Val	
210				720				725					730				
212	cag	atc	cga	ccc	atc	ttc	agc	aac	cgt	ggg	gat	ttc	cga	ggt	tac	tgc	2258
213	Gln	Ile	Arg	Pro	Ile	Phe	Ser	Asn	Arg	Gly	Asp	Phe	Arg	Gly	Tyr	Cys	
214				735			740					745					
216	tac	gtg	gag	ttt	aaa	gaa	gag	aaa	tca	gcc	ctt	cag	gca	ctg	gag	atg	2306
217	Tyr	Val	Glu	Phe	Lys	Glu	Glu	Lys	Ser	Ala	Leu	Gln	Ala	Leu	Glu	Met	
218	750				755					760					765		
220	gac	cgg	aaa	agt	gta	gaa	ggg	agg	cca	atg	ttt	gtt	tcc	ccc	tgt	gtg	2354
221	Asp	Arg	Lys	Ser	Val	Glu	Gly	Arg	Pro	Met	Phe	Val	Ser	Pro	Cys	Val	
222				770				775						780			
224	gat	aag	agc	aaa	aac	ccc	gat	ttt	aag	gtg	ttc	agg	tac	agc	act	tcc	2402
225	Asp	Lys	Ser	Lys	Asn	Pro	Asp	Phe	Lys	Val	Phe	Arg	Tyr	Ser	Thr	Ser	
226				785				790					795				
228	cta	gag	aaa	cac	aag	ctg	ttc	atc	tca	ggc	ctg	cct	ttc	tcc	tgt	act	2450
229	Leu	Glu	Lys	His	Lys	Leu	Phe	Ile	Ser	Gly	Leu	Pro	Phe	Ser	Cys	Thr	
230				800				805					810				
232	aaa	gag	gaa	cta	gaa	gaa	atc	tgt	aag	gct	cat	ggc	acc	gtg	aag	gac	2498
233	Lys	Glu	Glu	Leu	Glu	Glu	Ile	Cys	Lys	Ala	His	Gly	Thr	Val	Lys	Asp	
234				815			820					825					
236	ctc	agg	ctg	gtc	acc	aac	cgg	gct	ggc	aaa	cca	aag	ggc	ctg	gcc	tac	2546
237	Leu	Arg	Leu	Val	Thr	Asn	Arg	Ala	Gly	Lys	Pro	Lys	Gly	Leu	Ala	Tyr	
238	830				835					840					845		
240	gtg	gag	tat	gaa	aat	gaa	tcc	cag	gcg	tcg	cag	gct	gtg	atg	aag	atg	2594
241	Val	Glu	Tyr	Glu	Asn	Glu	Ser	Gln	Ala	Ser	Gln	Ala	Val	Met	Lys	Met	
242				850				855					860				
244	gac	ggc	atg	act	atc	aaa	gag	aac	atc	atc	aaa	gtg	gca	atc	agc	aac	2642
245	Asp	Gly	Met	Thr	Ile	Lys	Glu	Asn	Ile	Ile	Lys	Val	Ala	Ile	Ser	Asn	
246				865				870					875				
248	cct	cct	cag	agg	aaa	gtt	cca	gag	aag	cca	gag	acc	agg	aag	gca	cca	2690
249	Pro	Pro	Gln	Arg	Lys	Val	Pro	Glu	Lys	Pro	Glu	Thr	Arg	Lys	Ala	Pro	
250				880				885					890				
252	ggt	ggc	ccc	atg	ctt	ttg	ccg	cag	aca	tac	gga	gcg	agg	ggg	aag	gga	2738
253	Gly	Gly	Pro	Met	Leu	Leu	Pro	Gln	Thr	Tyr	Gly	Ala	Arg	Gly	Lys	Gly	
254				895			900					905					
256	agg	acg	cag	ctg	tct	cta	ctg	cct	cgt	gcc	ctg	cag	cgc	cca	agt	gct	2786
257	Arg	Thr	Gln	Leu	Ser	Leu	Leu	Pro	Arg	Ala	Leu	Gln	Arg	Pro	Ser	Ala	
258	910				915					920					925		
260	gca	gct	cct	cag	gct	gag	aac	ggc	cct	gcc	gcg	gct	cct	gca	gtt	gcc	2834
261	Ala	Ala	Pro	Gln	Ala	Glu	Asn	Gly	Pro	Ala	Ala	Ala	Pro	Ala	Val	Ala	
262				930				935						940			
264	gcc	cca	gca	gcc	acc	gag	gca	ccc	aag	atg	tcc	aat	gcc	gat	ttt	gcc	2882

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265 Ala Pro Ala Ala Thr Glu Ala Pro Lys Met Ser Asn Ala Asp Phe Ala
266          945          950          955
268 aag ctg ttt ctg aga aag tgaacgggac gctgggagac aggaaatgcc      2930
269 Lys Leu Phe Leu Arg Lys
270          960
272 ttacttcaact ctggccccggc ggacctccca ccaccagca gtgcactggg gatggacagg      2990
274 cctggtgtgc tgcgtgctcg caaccacaga tggctcctcg gctttagaca gaaaggggaa      3050
276 ggggttctaa gtcaagagcc tttcagtgt ccctcatatt gagggcagtg gcagaaaagt      3110
278 gaccactctg caggctgggc ccaggatgtg gtgtcctgag atagttttgt atcttaaaga      3170
280 ctgaggcaca gaagcgaaac gagaacacac tgtttttgag acacagttgt ccaaagtgtt      3230
282 ctggccagct ccggccccctt tttgtatgac acttctcttc caccctgcac agcacatgtg      3290
284 cccgtcattc ttttaatttt aaaagatgaa atggcagatg ctagtaattc acagaatggc      3350
286 ctcttggtgg ggtgggtctg aggggaagtca gctataaaac atttgctgga gttttgttca      3410
288 atggggctgt gcatttttat attatgtgtt tgtaaataac atgtcagccc ttgtttcatg      3470
290 tttcctaaaa gcagaatatt tgcaacattt gttttgtata ggaattattt gtgccacctg      3530
292 ctgtggactg ttttctttgc ctagtgacta gtgacctgtg ttgtctaaac atgagtttca      3590
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296 tattaactctg acgttctctt caaaacttct tgcgtgaatg tactcagatg tgcattcaca      3710
298 tacagatgtg ttttgaagtg ggtgtacctt gctttacctt atagatgtgt aaatagaact      3770
300 tttgtaagtc aaaaaaaaaa aaaaaaaaaa      3798
303 <210> SEQ ID NO: 2
304 <211> LENGTH: 963
305 <212> TYPE: PRT
306 <213> ORGANISM: Homo sapiens
308 <400> SEQUENCE: 2
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311 1          5          10          15
314 Lys Ala Gly Pro Lys Ala Asp Gly Glu Glu Asp Glu Val Lys Ala Ala
315          20          25          30
318 Arg Thr Arg Arg Lys Val Leu Ser Arg Ala Val Ala Ala Thr Tyr
319          35          40          45
322 Lys Thr Met Gly Pro Ala Trp Asp Gln Gln Glu Glu Gly Val Ser Glu
323          50          55          60
326 Ser Asp Gly Asp Glu Tyr Ala Met Ala Ser Ser Ala Glu Ser Ser Pro
327 65          70          75          80
330 Gly Glu Tyr Glu Trp Glu Tyr Asp Glu Glu Glu Glu Lys Asn Gln Leu
331          85          90          95
334 Glu Ile Glu Arg Leu Glu Glu Gln Leu Ser Ile Asn Val Tyr Asp Tyr
335          100         105         110
338 Asn Cys His Val Asp Leu Ile Arg Leu Leu Arg Leu Glu Gly Glu Leu
339          115         120         125
342 Thr Lys Val Arg Met Ala Arg Gln Lys Met Ser Glu Ile Phe Pro Leu
343          130         135         140
346 Thr Glu Glu Leu Trp Leu Glu Trp Leu His Asp Glu Ile Ser Met Ala
347 145         150         155         160
350 Gln Asp Gly Leu Asp Arg Glu His Val Tyr Asp Leu Phe Glu Lys Ala
351          165         170         175
354 Val Lys Asp Tyr Ile Cys Pro Asn Ile Trp Leu Glu Tyr Gly Gln Tyr
355          180         185         190

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## VERIFICATION SUMMARY

PATENT APPLICATION: US/09/763,985A

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Input Set : A:\0020-4817P.ST25.txt

Output Set: N:\CRF3\11212001\I763985A.raw

L:1126 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:53  
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L:1178 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:55  
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L:1334 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:61  
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